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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/303,510ADATE: 02/22/2000
TIME: 13:12:38

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This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: Collisson, Ellen W.
2 Hash, Stephen M.
3 Choi, InSoo
4 <120> TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
5 CTLA-4 Nucleic Acid and Polypeptides
6 <130> FILE REFERENCE: 54954
7 <140> CURRENT APPLICATION NUMBER: US/09/303,510A
8 <141> CURRENT FILING DATE: 1999-04-30
9 <150> EARLIER APPLICATION NUMBER: 60/083,869
10 <151> EARLIER FILING DATE: 1998-05-01
11 <160> NUMBER OF SEQ ID NOS: 83
12 <170> SOFTWARE: PatentIn Ver. 2.1
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14 <211> LENGTH: 941
15 <212> TYPE: DNA
16 <213> ORGANISM: Feline
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19 ccgctcttga tgctagctag tcttttttac ttctgttcag gtatcatcca ggtgaacaag 120
20 acagtggaag aagtagcagt actatcctgt gattacaaca tttccaccaa agaactgacg 180
21 gaaattcgaa tctattggca aaaggatgat gaaatggtgt tggctgtcat gtctggcaaa 240
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26 atgtgcttaa cttctggagg ttttccaaag cctcacctct cctggctgga aaatgaagaa 540
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29 ggaaacttac tagtatcaca gatcttcaac tggcaaaaat cagagccaca gccttctaata 720
30 aatcagctct ggatcattat cctgagctca gtagtaagtg ggattgttgt gatcactgca 780
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32 agagcgcgga aatggaaaag atctcacctg tctacataga ttctgcagaa ccactgtatg 900
33 cagagcatct ggaggtagcc tcttagctc ttctctacta g 941
34 <210> SEQ ID NO 2
35 <211> LENGTH: 292
36 <212> TYPE: PRT
37 <213> ORGANISM: Feline
38 <400> SEQUENCE: 2
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40 1 5 10 15
41 Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys
42 20 25 30
43 Ser Gly Ile Ile Gln Val Asn Lys Thr Val Glu Glu Val Ala Val Leu
44 35 40 45
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45      Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile
46          50                      55                      60
47      Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys
48          65                      70                      75                      80
49      Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr
50          85                      90                      95
51      Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
52          100                     105                     110
53      Lys Tyr Thr Cys Ile Ile Gln Lys Ile Glu Lys Gly Ser Tyr Lys Val
54          115                     120                     125
55      Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val
56          130                     135                     140
57      Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile
58          145                     150                     155                     160
59      Met Cys Leu Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Leu
60          165                     170                     175
61      Glu Asn Glu Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
62          180                     185                     190
63      Pro Glu Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Met
64          195                     200                     205
65      Thr Asn Asn His Ser Phe Leu Cys Leu Val Lys Tyr Gly Asn Leu Leu
66          210                     215                     220
67      Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn
68          225                     230                     235                     240
69      Asn Gln Leu Trp Ile Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val
70          245                     250                     255
71      Val Ile Thr Ala Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala
72          260                     265                     270
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79 <212> TYPE: DNA

80 <213> ORGANISM: Feline

81 <400> SEQUENCE: 3

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84      acagtggaaag aagtagcagt actatcctgt gattacaaca tttccaccaa agaactgacg 180
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89      gacttccttg tccctagtat aactgatctt ggaaatccat ctcataacat caaaaggata 480
90      atgtgcttaa cttctggagg ttttccaaag cctcacctct cctggctgga aaatgaagaa 540
91      gaattaaatg ccatcaacac aacagtttcc caagatcctg aaactgagct ctacactatt 600
92      agcagtgaac tggatttcaa tatgacaaac aaccatagct tcctgtgtct tgtcaagtat 660
93      ggaaacttaa tagtatcaca gatcttcaac tggcaaaaat cagagccaca gccttcta 720
94      aatcagctct ggatcattat cctgagctca gtagtaagtg ggattgtgt gatcactgca 780

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99      <212> TYPE: PRT
100     <213> ORGANISM: Feline
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104     Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys
105     20          25          30
106     Ser Gly Ile Ile Gln Val Asn Lys Thr Val Glu Glu Val Ala Val Leu
107     35          40          45
108     Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile
109     50          55          60
110     Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys
111     65          70          75          80
112     Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr
113     85          90          95
114     Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
115     100         105         110
116     Lys Tyr Thr Cys Ile Ile Gln Lys Ile Gln Lys Gly Ser Tyr Lys Val
117     115         120         125
118     Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val
119     130         135         140
120     Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile
121     145         150         155         160
122     Met Cys Leu Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Leu
123     165         170         175
124     Glu Asn Glu Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
125     180         185         190
126     Pro Glu Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Met
127     195         200         205
128     Thr Asn Asn His Ser Phe Leu Cys Leu Val Lys Tyr Gly Asn Leu Ile
129     210         215         220
130     Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn
131     225         230         235         240
132     Asn Gln Leu Trp Ile Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val
133     245         250         255
134     Val Ile Thr Ala Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala
135     260         265         270
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137     275         280         285
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139     290
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141     <211> LENGTH: 1080
142     <212> TYPE: DNA
143     <213> ORGANISM: Feline
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145      gtttctgtgt tcctcgggaa tgtcactgag cttatacatc tgggtctctgg gagctgcagt 60
146      ggatgggcat ttgtgacagc actatgggac tgagtcacac tctccttctg atggccctcc 120
147      tgctctctgg tgtttcttcc atgaagagtc aagcatattt caacaagact ggagaactgc 180
148      catgccattht tacaaactct caaaacataa gcctggatga gctggtagta ttttggcagg 240
149      accaggataa gctggttctg tatgagatat tcagaggcaa agagaaccct caaaatgttc 300
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151      atgttcagat caaggacaa ggcacatata actgtttcat tcattataaa gggcccaaag 420
152      gactagtthc catgcaccaa atgagttctg acctatcagt gcttgctaac ttcagtcaac 480
153      ctgaaataac agtaacttct aatagaacag aaaattctgg catcataaat ttgacctgct 540
154      catctataca aggttaccca gaacctaaag agatgtattht tcagctaaac actgagaatt 600
155      caactactaa gtatgatact gtcatagaaga aatctcaaaa taatgtgaca gaactgtaca 660
156      acgtttctat cagcttgccct ttttcagtcc ctgaagcaca caatgtgagc gtcttttctg 720
157      ccttgaaact ggagacactg gagatgctgc tctccctacc tttcaatata gatgcacaac 780
158      ctaaggataa agacctgaa caaggccact tctctggat tgcggctgta cttgtaattgt 840
159      ttgttgthtt ttgtgggatg gtgtccttta aaactactaa gaaaaggaaag aagaagcagc 900
160      ctggcccttc tcatgaatgt gaaacctca aaaggagag aaaagagagc aaacagacca 960
161      acgaaagagt accataccac gtacctgaga gatctgatga agcccagtg gttaacattht 1020
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165 <212> TYPE: PRT

166 <213> ORGANISM: Feline

167 <400> SEQUENCE: 6

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171      20          25          30
172      Phe Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Gln Asn
173      35          40          45
174      Ile Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys Leu
175      50          55          60
176      Val Leu Tyr Glu Ile Phe Arg Gly Lys Glu Asn Pro Gln Asn Val His
177      65          70          75          80
178      Leu Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu
179      85          90          95
180      Arg Leu His Asn Val Gln Ile Lys Asp Lys Gly Thr Tyr His Cys Phe
181      100         105         110
182      Ile His Tyr Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met Ser
183      115         120         125
184      Ser Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Thr Val
185      130         135         140
186      Thr Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys Ser
187      145         150         155         160
188      Ser Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn
189      165         170         175
190      Thr Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln
191      180         185         190
192      Asn Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser
193      195         200         205
194      Val Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu

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195          210          215          220
196      Thr Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro
197      225          230          235          240
198      Lys Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val
199          245          250          255
200      Leu Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu
201          260          265          270
202      Arg Lys Arg Lys Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr
203          275          280          285
204      Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro
205          290          295          300
206      Tyr His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Val Asn Ile Leu
207          305          310          315          320
208      Lys Thr Ala Ser Gly Asp Lys Asn Gln
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211 <211> LENGTH: 688
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217      tgcaagtaca ctcacaactt cttctcaaag gagttccggg catcccttta taaggagta 180
218      gatagtgtcg tggaagtctg cgttgtgaat ggaaattact cccatcagcc tcagttctac 240
219      tcaagtacag gattcgactg tgatgggaaa ttgggcaatg aaacagtgac attctacctc 300
220      cgaaatttgt ttgttaacca aacggatatt tacttctgca aaattgaagt catgtatcca 360
221      cctccttaca tagacaatga gaagagcaat gggaccatta tccacgtgaa agagaaacat 420
222      ctttgtccag ctcagctgtc tcctgaatct tccaagccat tttgggcact ggtggtggtt 480
223      ggtggaatcc taggtttcta cagcttgcta gcaacagtgg ctcttggtgc ttgctggatg 540
224      aagaccaaga ggagtaggat ccttcagagt gactatatga acatgacccc ccggaggcca 600
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226      tcctgacatg gaccttatc cagaagcc 688
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228 <211> LENGTH: 221
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234      Val Thr Glu Asn Lys Ile Leu Val Lys Gln Leu Pro Arg Leu Val Val
235          20          25          30
236      Tyr Asn Asn Glu Val Asn Leu Ser Cys Lys Tyr Thr His Asn Phe Phe
237          35          40          45
238      Ser Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asp Ser Ala Val
239          50          55          60
240      Glu Val Cys Val Val Asn Gly Asn Tyr Ser His Gln Pro Gln Phe Tyr
241          65          70          75          80
242      Ser Ser Thr Gly Phe Asp Cys Asp Gly Lys Leu Gly Asn Glu Thr Val
243          85          90          95
244      Thr Phe Tyr Leu Arg Asn Leu Phe Val Asn Gln Thr Asp Ile Tyr Phe

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VERIFICATION SUMMARY
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